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**Search Results - Record(s) 1 through 6 of 6 returned.**☐ 1. Document ID: US 5869258 A

L7: Entry 1 of 6

File: USPT

Feb 9, 1999

US-PAT-NO: 5869258

DOCUMENT-IDENTIFIER: US 5869258 A

TITLE: Detection system for mutagens that identifies mutagenic changes

DATE-ISSUED: February 9, 1999

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gee; Pauline	Berkeley	CA		
Maron; Dorothy M.	Orinda	CA		
Ames; Bruce N.	Berkeley	CA		

US-CL-CURRENT: 435/6; 435/252.3, 435/252.8, 435/29

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMIC	Draw Desc	Image
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☐ 2. Document ID: US 5712386 A

L7: Entry 2 of 6

File: USPT

Jan 27, 1998

US-PAT-NO: 5712386

DOCUMENT-IDENTIFIER: US 5712386 A

TITLE: Kits for detecting a target nucleic acid with blocking oligonucleotides

DATE-ISSUED: January 27, 1998

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wang; Chang-Ning J.	Chelmsford	MA		
Wu; Kai-Yuan	Lowell	MA		

US-CL-CURRENT: 536/24.33; 435/6, 435/91.2, 536/23.1, 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Claims	KMIC	Draw Desc	Image
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☐ 3. Document ID: US 5681737 A

L7: Entry 3 of 6

File: USPT

Oct 28, 1997

US-PAT-NO: 5681737

DOCUMENT-IDENTIFIER: US 5681737 A

TITLE: Detection system for mutagens that also identifies mutagenic changes

DATE-ISSUED: October 28, 1997

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gee; Pauline	Berkeley	CA		
Maron; Dorothy M.	Orinda	CA		
Ames; Bruce N.	Berkeley	CA		

US-CL-CURRENT: 435/252.3; 435/252.8, 435/320.1, 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference
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KMIC	Draw Desc	Image
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☐ 4. Document ID: US 5627054 A

L7: Entry 4 of 6

File: USPT

May 6, 1997

US-PAT-NO: 5627054

DOCUMENT-IDENTIFIER: US 5627054 A

TITLE: Competitor primer asymmetric polymerase chain reaction

DATE-ISSUED: May 6, 1997

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Gillespie, deceased; David	late of Glenmore	PA		

US-CL-CURRENT: 435/91.2; 536/24.3

Full	Title	Citation	Front	Review	Classification	Date	Reference
------	-------	----------	-------	--------	----------------	------	-----------

KMIC	Draw Desc	Image
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☐ 5. Document ID: US 5567583 A

L7: Entry 5 of 6

File: USPT

Oct 22, 1996

US-PAT-NO: 5567583

DOCUMENT-IDENTIFIER: US 5567583 A

TITLE: Methods for reducing non-specific priming in DNA detection

DATE-ISSUED: October 22, 1996

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Wang; Chang-Ning J.	Chelmsford	MA		
Wu; Kai-Yuan	Lowell	MA		

US-CL-CURRENT: 435/6; 435/91.2

Full	Title	Citation	Front	Review	Classification	Date	Reference
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KWIC	Draw Desc	Image
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☐ 6. Document ID: US 5075216 A

L7: Entry 6 of 6

File: USPT

Dec 24, 1991

US-PAT-NO: 5075216

DOCUMENT-IDENTIFIER: US 5075216 A

TITLE: Methods for DNA sequencing with thermus aquaticus DNA polymerase

DATE-ISSUED: December 24, 1991

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Innis; Michael A.	Moraga	CA		
Myambo; Kenneth B.	Pittsburg	CA		
Gelfand; David H.	Oakland	CA		
Brow; Mary Ann D.	Oakland	CA		

US-CL-CURRENT: 435/6; 435/5, 435/810, 435/91.2, 436/501, 436/808, 536/24.33,  
536/26.26, 536/27.14, 536/28.2

Full	Title	Citation	Front	Review	Classification	Date	Reference
------	-------	----------	-------	--------	----------------	------	-----------

KWIC	Draw Desc	Image
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Generate Collection

Term	Documents
LABES2	0
LABE.DWPI,EPAB,JPAB,USPT.	138
LABEAL.DWPI,EPAB,JPAB,USPT.	1
LABEAN.DWPI,EPAB,JPAB,USPT.	15
LABEAU.DWPI,EPAB,JPAB,USPT.	47
LABECH.DWPI,EPAB,JPAB,USPT.	1
LABECK.DWPI,EPAB,JPAB,USPT.	1
LABECO.DWPI,EPAB,JPAB,USPT.	44
LABED.DWPI,EPAB,JPAB,USPT.	10
LABEDA.DWPI,EPAB,JPAB,USPT.	133
(L6 AND (LABES2 OR MARK\$2 OR DYES2) ) .USPT,JPAB,EPAB,DWPI.	6

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09/3-5, 89

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NEWS 13 Sep 17 IMSworld Pharmaceutical Company Directory name change  
to PHARMASEARCH  
NEWS 14 Oct 09 Korean abstracts now included in Derwent World Patents  
Index  
NEWS 15 Oct 09 Number of Derwent World Patents Index updates increased  
NEWS 16 Oct 15 Calculated properties now in the REGISTRY/ZREGISTRY File  
NEWS 17 Oct 22 Over 1 million reactions added to CASREACT  
NEWS 18 Oct 22 DGENE GETSIM has been improved  
NEWS 19 Oct 29 AAASD no longer available  
NEWS 20 Nov 19 New Search Capabilities USPATFULL and USPAT2  
NEWS 21 Nov 19 TOXCENTER(SM) - new toxicology file now available on STN  
NEWS 22 Nov 29 COPPERLIT now available on STN  
NEWS 23 Nov 29 DWPI revisions to NTIS and US Provisional Numbers  
  
NEWS EXPRESS August 15 CURRENT WINDOWS VERSION IS V6.0c,  
CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP),  
AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001  
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=> s fluorescence correlation spectroscopy and (asymmetric PCR or asymmetric amplifications)

L1 5 FLUORESCENCE CORRELATION SPECTROSCOPY AND (ASYMMETRIC PCR OR ASYMMETRIC AMPLIFICATIONS)

=> s l1 and ratio#

L2 0 L1 AND RATIO#

=> s l1 and (label## or mark## or dye##)

L3 5 L1 AND (LABEL## OR MARK## OR DYE##)

=> dup rem l3

PROCESSING COMPLETED FOR L3

L4 3 DUP REM L3 (2 DUPLICATES REMOVED)

=> d l4 1-3 bib ab kwic

L4 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS

AN 2000:408543 CAPLUS

DN 133:40268

TI Method for quantitative analysis of the target nucleic acid by  
**asymmetric PCR and fluorescence correlation spectroscopy**

IN Kinjo, Seikou; Kaneki, Masataka

PA Japan

SO Jpn. Kokai Tokkyo Koho, 12 pp.

CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	JP 2000166599	A2	20000620	JP 1998-353254	19981211
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AB A method for quant. anal. of the target nucleic acid by asym. PCR and **fluorescence correlation spectroscopy** (FCS), without a need for sepn. of free and bound **label**, is disclosed. Nucleic acid amplification is carried out with a pair of primers, one **labeled** and the other unlabeled. The **label** is preferably a fluorescent **label**, and unlabeled primers are in excess. The method also comprises the steps of obtaining multiple data measurement within a limited 3D visual field on the soln. mobility/fluctuation of the **label**, and quantification of the target nucleic acid. Statistical anal. of the data by performing arithmetic operations using the autocorrelation function is also included. The limited 3D visual field is diffraction limited range formed by confocal optics. Single photon measurement mode is used. The method was applied to the quant. anal. of lambda phage DNA using a rhodamine

- labeled primers.
- TI Method for quantitative analysis of the target nucleic acid by  
**asymmetric PCR and fluorescence  
correlation spectroscopy**
- AB A method for quant. anal. of the target nucleic acid by asym. PCR and  
**fluorescence correlation spectroscopy (FCS)**,  
without a need for sepn. of free and bound **label**, is disclosed.  
Nucleic acid amplification is carried out with a pair of primers, one  
**labeled** and the other unlabeled. The **label** is  
preferably a fluorescent **label**, and unlabeled primers are in  
excess. The method also comprises the steps of obtaining multiple data  
measurement within a limited 3D visual field on the soln.  
mobility/fluctuation of the **label**, and quantification of the  
target nucleic acid. Statistical anal. of the data by performing  
arithmetic operations using the autocorrelation function is also included.  
The limited 3D visual field is diffraction limited range formed by  
confocal optics. Single photon measurement mode is used. The method was  
applied to the quant. anal. of lambda phage DNA using a rhodamine  
**labeled** primers.
- ST nucleic acid quantification arithmetic statistics microscope; DNA  
amplification asym PCR **fluorescence correlation  
spectroscopy**
- IT PCR (polymerase chain reaction)  
(asym.; method and app. for quant. anal. of target nucleic acid by  
polymerase chain reaction and **fluorescence  
correlation spectroscopy**)
- IT Fluorometry  
(correlation, (FCS); method and app. for quant. anal. of target nucleic  
acid by polymerase chain reaction and **fluorescence  
correlation spectroscopy**)
- IT Mathematical methods  
(curve, for dynamics of the **label**, anal. of; method and app.  
for quant. anal. of target nucleic acid by polymerase chain reaction  
and **fluorescence correlation spectroscopy**  
)
- IT Primers (nucleic acid)  
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL  
(Biological study); PROC (Process); USES (Uses)  
(**labeled**; method and app. for quant. anal. of target nucleic  
acid by polymerase chain reaction and **fluorescence  
correlation spectroscopy**)
- IT Algorithm  
Autocorrelation function  
Fluorescent indicators  
Fluorescent probes  
Microscopes  
Nucleic acid amplification (method)  
Statistical analysis  
(method and app. for quant. anal. of target nucleic acid by polymerase  
chain reaction and **fluorescence correlation  
spectroscopy**)
- IT Nucleic acids  
RL: ANT (Analyte); ANST (Analytical study)  
(method and app. for quant. anal. of target nucleic acid by polymerase  
chain reaction and **fluorescence correlation  
spectroscopy**)
- IT Primers (nucleic acid)  
RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL  
(Biological study); PROC (Process); USES (Uses)  
(method and app. for quant. anal. of target nucleic acid by polymerase  
chain reaction and **fluorescence correlation  
spectroscopy**)
- IT Diffusion  
(of **label** in soln., measurement of; method and app. for

quant. anal. of target nucleic acid by polymerase chain reaction and **fluorescence correlation spectroscopy**)

IT 146368-16-3, Cy3  
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
 (Cy3; method and app. for quant. anal. of target nucleic acid by polymerase chain reaction and **fluorescence correlation spectroscopy**)

IT 146368-14-1, Cy5  
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
 (Cy5; method and app. for quant. anal. of target nucleic acid by polymerase chain reaction and **fluorescence correlation spectroscopy**)

IT 81-88-9 13558-31-1 27072-45-3, FITC 47165-04-8, DAPI 169799-14-8, Cy7 172777-84-3, Cy5.5 189767-45-1, Cy3.5  
 RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
 (method and app. for quant. anal. of target nucleic acid by polymerase chain reaction and **fluorescence correlation spectroscopy**)

L4 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS

AN 2000:275403 CAPLUS

DN 132:304266

TI Quantitative determination of target nucleic acid by **asymmetric PCR and fluorescence correlation spectroscopy**

IN Kinjo, Masataka

PA Japan

SO Ger. Offen., 18 pp.

CODEN: GWXXBX

DT Patent

LA German

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 19950823	A1	20000427	DE 1999-19950823	19991021
	JP 2000125900	A2	20000509	JP 1998-301316	19981022
PRAI	JP 1998-301316		19981022		

AB The invention concerns a quant. procedure for target nucleic acid detection using a amplification reaction and a **labeled** primer. No sepn. of free and hybridized **labeled** DNA is necessary. Thus, a PCR reaction using a non-tagged first primer and a fluorescence-tagged second primer, present in fewer copies than the first primer, is carried out. The reaction may be followed by **fluorescence correlation spectroscopy**. These results are statistically analyzed and used to det. the no. of target nucleic acids in the sample.

TI Quantitative determination of target nucleic acid by **asymmetric PCR and fluorescence correlation spectroscopy**

AB The invention concerns a quant. procedure for target nucleic acid detection using a amplification reaction and a **labeled** primer. No sepn. of free and hybridized **labeled** DNA is necessary. Thus, a PCR reaction using a non-tagged first primer and a fluorescence-tagged second primer, present in fewer copies than the first primer, is carried out. The reaction may be followed by **fluorescence correlation spectroscopy**. These results are statistically analyzed and used to det. the no. of target nucleic acids in the sample.

ST asym PCR **fluorescence correlation spectroscopy**  
 DNA quantitation

IT PCR (polymerase chain reaction)

(asym.; quant. detn. of target nucleic acid by asym. PCR and  
**fluorescence correlation spectroscopy**)

IT Fluorometry  
(correlation; quant. detn. of target nucleic acid by asym. PCR and  
**fluorescence correlation spectroscopy**)

IT Primers (nucleic acid)  
RL: ARG (Analytical reagent use); BPR (Biological process); ANST  
(Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)  
(fluorophore-labeled; quant. detn. of target nucleic acid by  
asym. PCR and **fluorescence correlation  
spectroscopy**)

IT DNA  
RL: ANT (Analyte); ANST (Analytical study)  
(quant. detn. of target nucleic acid by asym. PCR and  
**fluorescence correlation spectroscopy**)

IT 13558-31-1D, conjugates with primers 27072-45-3D, FITC, conjugates with  
primers 47165-04-8D, DAPI, conjugates with primers 146397-20-8D, Cy3,  
conjugates with primers 169799-14-8D, Cy7, conjugates with primers  
172777-84-3D, Cy5.5, conjugates with primers 189767-45-1D, Cy3.5,  
conjugates with primers  
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)  
(quant. detn. of target nucleic acid by asym. PCR and  
**fluorescence correlation spectroscopy**)

IT 264902-73-0, 1: PN: DE19950823 SEQID: 8 unclaimed DNA 264902-74-1, 2:  
PN: DE19950823 SEQID: 9 unclaimed DNA  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; quant. detn. of target nucleic acid by  
asym. PCR and **fluorescence correlation  
spectroscopy**)

L4 ANSWER 3 OF 3 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 1  
AN 1998:490523 BIOSIS  
DN PREV199800490523  
TI Detection of **asymmetric PCR** products in homogeneous  
solution by **fluorescence correlation  
spectroscopy**.  
AU Kinjo, Masataka (1)  
CS (1) Lab. Biophysics, Res. Inst. Electronic Sci., Hokkaido Univ., 060  
Sapporo Japan  
SO Biotechniques, (Oct., 1998) Vol. 25, No. 4, pp. 706-715.  
ISSN: 0736-6205.  
DT Article  
LA English  
AB The yield of the double-stranded DNA product (500 bp) of  
**asymmetric PCR** with a rhodamine-labeled primer  
(Rho-primer) was determined in a homogeneous solution using  
**fluorescence correlation spectroscopy** (FCS).  
FCS provides the average number of molecules in a focused volume and the  
diffusion constant that relates the molecular weight. Since FCS measures  
the fluctuation of fluorescence intensity in a very small sample volume,  
the reaction mixture was directly placed on the FCS optical field without  
any purification procedure after amplification. The result of changing the  
initial number of templates suggested that elongation of the Rho-primer  
could be detected by FCS in a PCR mixture containing a single copy of the  
target gene in the initial condition. Possible scientific applications and  
perspectives of the proposed approach are discussed.

TI Detection of **asymmetric PCR** products in homogeneous  
solution by **fluorescence correlation  
spectroscopy**.

AB The yield of the double-stranded DNA product (500 bp) of  
**asymmetric PCR** with a rhodamine-labeled primer  
(Rho-primer) was determined in a homogeneous solution using  
**fluorescence correlation spectroscopy** (FCS).  
FCS provides the average number of molecules in a focused volume and the

*Can't use it  
because the date has to be  
one year if they are  
the same not invent*



diffusion constant that relates the molecular. . .

IT Methods & Equipment

**fluorescence correlation spectroscopy:**

analytical method, spectroscopic techniques: CB; PCR [polymerase chain reaction]: DNA amplification, in-situ recombinant gene expression detection, molecular genetic method, sequencing. . .

=>

L5 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2001 ACS

AN 2000:408543 CAPLUS

DN 133:40268

TI Method for quantitative analysis of the target nucleic acid by  
**asymmetric PCR** and fluorescence correlation spectroscopy

IN Kinjo, Seikou; Kaneki, Masataka

PA Japan

SO Jpn. Kokai Tokkyo Koho, 12 pp.

CODEN: JKXXAF

DT Patent

LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2000166599	A2	20000620	JP 1998-353254	19981211
AB	A method for quant. anal. of the target nucleic acid by asym. PCR and fluorescence correlation spectroscopy (FCS), without a need for sepn. of free and bound label, is disclosed. Nucleic acid amplification is carried out with a pair of <b>primers</b> , one <b>labeled</b> and the other unlabeled. The <b>label</b> is preferably a fluorescent <b>label</b> , and unlabeled <b>primers</b> are in excess. The method also comprises the steps of obtaining multiple data measurement within a limited 3D visual field on the soln. mobility/fluctuation of the label, and quantification of the target nucleic acid. Statistical anal. of the data by performing arithmetic operations using the autocorrelation function is also included. The limited 3D visual field is diffraction limited range formed by confocal optics. Single photon measurement mode is used. The method was applied to the quant. anal. of lambda phage DNA using a rhodamine <b>labeled primers</b> .				
TI	Method for quantitative analysis of the target nucleic acid by <b>asymmetric PCR</b> and fluorescence correlation spectroscopy				
AB	A method for quant. anal. of the target nucleic acid by asym. PCR and fluorescence correlation spectroscopy (FCS), without a need for sepn. of free and bound label, is disclosed. Nucleic acid amplification is carried out with a pair of <b>primers</b> , one <b>labeled</b> and the other unlabeled. The <b>label</b> is preferably a fluorescent <b>label</b> , and unlabeled <b>primers</b> are in excess. The method also comprises the steps of obtaining multiple data measurement within a limited 3D visual field on the soln. mobility/fluctuation of the label, and quantification of the target nucleic acid. Statistical anal. of the data by performing arithmetic operations using the autocorrelation function is also included. The limited 3D visual field is diffraction limited range formed by confocal optics. Single photon measurement mode is used. The method was applied to the quant. anal. of lambda phage DNA using a rhodamine <b>labeled primers</b> .				
IT	<b>Primers</b> (nucleic acid) RL: BPR (Biological process); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses) ( <b>labeled</b> ; method and app. for quant. anal. of target nucleic acid by polymerase chain reaction and fluorescence correlation spectroscopy)				

L5 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2001 ACS

AN 2000:275403 CAPLUS

DN 132:304266

TI Quantitative determination of target nucleic acid by **asymmetric PCR** and fluorescence correlation spectroscopy

IN Kinjo, Masataka

PA Japan

SO Ger. Offen., 18 pp.

CODEN: GWXXBX

DT Patent

LA German

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	DE 19950823	A1	20000427	DE 1999-19950823	19991021
	JP 2000125900	A2	20000509	JP 1998-301316	19981022
PRAI	JP 1998-301316		19981022		
AB	The invention concerns a quant. procedure for target nucleic acid detection using a amplification reaction and a <b>labeled primer</b> . No sepn. of free and hybridized labeled DNA is necessary. Thus, a PCR reaction using a non-tagged first primer and a fluorescence-tagged second primer, present in fewer copies than the first primer, is carried out. The reaction may be followed by fluorescence correlation spectroscopy. These results are statistically analyzed and used to det. the no. of target nucleic acids in the sample.				
TI	Quantitative determination of target nucleic acid by <b>asymmetric PCR</b> and fluorescence correlation spectroscopy				
AB	The invention concerns a quant. procedure for target nucleic acid detection using a amplification reaction and a <b>labeled primer</b> . No sepn. of free and hybridized labeled DNA is necessary. Thus, a PCR reaction using a non-tagged first primer and a fluorescence-tagged second primer, present in fewer copies than the first primer, is carried out. The reaction may be followed by fluorescence correlation spectroscopy. These results are statistically analyzed and used to det. the no. of target nucleic acids in the sample.				
IT	<b>Primers</b> (nucleic acid) RL: ARG (Analytical reagent use); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses) (fluorophore- <b>labeled</b> ; quant. detn. of target nucleic acid by asym. PCR and fluorescence correlation spectroscopy)				
L5	ANSWER 3 OF 11		MEDLINE	DUPLICATE 1	
AN	2000107151		MEDLINE		
DN	20107151		PubMed ID: 10639495		
TI	PCR-derived ssDNA probes for fluorescent in situ hybridization to HIV-1 RNA.				
AU	Knuchel M C; Graf B; Schlaepfer E; Kuster H; Fischer M; Weber R; Cone R W				
CS	Division of Infectious Diseases, Department of Internal Medicine, University Hospital Zurich, Zurich, Switzerland.				
SO	JOURNAL OF HISTOCHEMISTRY AND CYTOCHEMISTRY, (2000 Feb) 48 (2) 285-94. Journal code: IDZ; 9815334. ISSN: 0022-1554.				
CY	United States				
DT	Journal; Article; (JOURNAL ARTICLE)				
LA	English				
FS	Priority Journals				
EM	200002				
ED	Entered STN: 20000314				
	Last Updated on STN: 20000314				
	Entered Medline: 20000229				
AB	We developed a simple and rapid technique to synthesize single-stranded DNA (ssDNA) probes for fluorescent in situ hybridization (ISH) to human immunodeficiency virus 1 (HIV-1) RNA. The target HIV-1 regions were amplified by the polymerase chain reaction (PCR) and were simultaneously labeled with dUTP. This product served as template for an optimized <b>asymmetric PCR</b> (one-primer PCR) that incorporated digoxigenin (dig)- <b>labeled</b> dUTP. The input DNA was subsequently digested by uracil DNA glycosylase, leaving intact, single-stranded, digoxigenin-labeled DNA probe. A cocktail of ssDNA probes representing 55% of the HIV-1 genome was hybridized to HIV-1-infected 8E5 T-cells and uninfected H9 T-cells. For comparison, parallel hybridizations were done with a plasmid-derived RNA probe mix covering 85% of the genome and a PCR-derived RNA probe mix covering 63% of the genome. All three probe types produced bright signals, but the best signal-to-noise ratios and the highest sensitivities were obtained with the ssDNA probe. In addition, the ssDNA probe syntheses generated large amounts of probe (0.5				

to 1 microg ssDNA probe per synthesis) and were easier to perform than the RNA probe syntheses. These results suggest that ssDNA probes may be preferable to RNA probes for fluorescent ISH. (J Histochem Cytochem 48:285-293, 2000)

AB . . . by the polymerase chain reaction (PCR) and were simultaneously labeled with dUTP. This product served as template for an optimized **asymmetric PCR** (one-primer PCR) that incorporated digoxigenin (dig)-labeled dUTP. The input DNA was subsequently digested by uracil DNA glycosylase, leaving intact, single-stranded, digoxigenin-labeled DNA probe. A cocktail of. . .

L5 ANSWER 4 OF 11 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2000:4853 BIOSIS

DN PREV200000004853

TI Detection of Escherichia coli O157:H7 DNA using two fluorescence polarization methods.

AU Ye, Bang-Ce (1); Ikebukuro, Kazunori; Karube, Isao

CS (1) Key State Laboratory of Bioreactor Engineering, Research Institute of Biochemistry, East China University of Science and Technology, MeiLong Road 130, 200237, Shanghai China

SO Fresenius' Journal of Analytical Chemistry, (Nov., 1999) Vol. 365, No. 5, pp. 452-457.

ISSN: 0937-0633.

DT Article

LA English

SL English

AB Using stx 2 gene in verotoxin-producing Escherichia coli O157:H7 as a target DNA, polymerase chain reaction (PCR) amplification has been combined with fluorescence polarization (FP) by two distinct combination protocols. The first approach (PCR-probe-FP) requires that fluorescence labeled specific probes are hybridized with the **asymmetric PCR** product. In the second protocol (PCR-primer-FP), the fluorescence labeled primer is used in PCR amplification. In both methods, the PCR products are detected using fluorescence polarization. Hybridization (in the PCR-probe-FP method) and conversion (in the PCR-primer-FP method) of 5'-fluorescence labeled oligodeoxynucleotide to the PCR product are monitored by an increase in the anisotropy ratio. The results demonstrate the importance of **asymmetric PCR** (in the first method) and the selection of dye-modified primer concentration (in the second method) for designing a polarization strategy for the detection of DNA sequence. It has been found that the methods can be used for the identification of infectious agents. This system has also been applied to the determination of Escherichia coli O157:H7 strains.

AB. . . (FP) by two distinct combination protocols. The first approach (PCR-probe-FP) requires that fluorescence labeled specific probes are hybridized with the **asymmetric PCR** product. In the second protocol (PCR-primer-FP), the fluorescence labeled primer is used in PCR amplification. In both methods, the PCR products are detected using fluorescence polarization. Hybridization (in the PCR-probe-FP method) and conversion (in the PCR-primer-FP method) of 5'-fluorescence labeled oligodeoxynucleotide to the PCR product are monitored by an increase in the anisotropy ratio. The results demonstrate the importance of **asymmetric PCR** (in the first method) and the selection of dye-modified primer concentration (in the second method) for designing a polarization strategy for the detection of DNA sequence. It has been found. . .

L5 ANSWER 5 OF 11 MEDLINE

AN 2000189615 MEDLINE

DN 20189615 PubMed ID: 10727081

TI DENS (differential extension with nucleotide subsets): application to the sequencing of human genomic DNA and cDNA.

AU Zevin-Sonkin D; Liberzon A; Chochikyan A; Hovhannisyan H; Lvovsky L;  
 Ulanovsky L  
 CS Department of Structural Biology, Weizmann Institute of Science, Rehovot,  
 Israel.  
 SO DNA SEQUENCE, (1999) 10 (4-5) 245-54.  
 Journal code: A9H; 9107800. ISSN: 1042-5179.  
 CY Switzerland  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 200004  
 ED Entered STN: 20000421  
 Last Updated on STN: 20000421  
 Entered Medline: 20000412  
 AB Here we describe further development of our method of DNA sequencing by  
 Differential Extension with Nucleotide Subsets (DENS) and its application  
 to the sequencing of human genomic DNA and full-insert cDNA. Essentially,  
 DENS is primer walking without custom primer synthesis; instead, DENS uses  
 a presynthesized library of octamer primers degenerate in two positions  
 (4,096 tubes/sequences for a complete library). DENS converts an octamer  
 selected from this library into a long primer on the template, at the  
 intended site only. This is done using a two-step procedure which starts  
 with a limited extension of the octamer (at 20 degrees C) in the presence  
 of only two of the four possible dNTPs. The primer is extended by five  
 bases or more at the intended priming site, which is deliberately selected  
 to maximize the extension length (as are the two-dNTP set and the primer  
 itself). The subsequent termination reaction at 60 degrees C then accepts  
 the primer extended at the intended site, but not at alternative sites,  
 where the initial extension (if any) is generally much shorter. This paper  
 presents a set of rules for selection of DENS priming sites. We also  
 compare different ways of template preparation for DENS sequencing. The  
 data were obtained from primer walking on three human genomic DNA  
 subclones of 3 to 4 kbp and four cDNA clones containing inserts of 1.9,  
 2.3, 3.8, and 4.9 kbp. Full-length sequences were obtained from both  
 strands of each subclone by automated **dye**-terminator fluorescent  
 DNA sequencing using DENS with degenerate octamer **primers**. We  
 compared the following types of DNA templates: single-stranded and  
 double-stranded phagemid DNA, double-stranded PCR products,  
**asymmetric PCR** products, and single-stranded DNA  
 produced by digestion with Lambda Exonuclease of double-stranded PCR  
 product phosphorylated at one end (Exo-PCR). While all of the preps were  
 found to work, the best results were obtained with Exo-PCR and phagemid  
 single-stranded DNA. Exo-PCR directly from overnight bacterial culture  
 with no plasmid prep of any kind yielded templates for DENS as good as  
 Exo-PCR from purified DNA. We found that the Tm of the differentially  
 extended octamers is an important factor in the success of DENS.  
 Clustering of successful reactions was clearly distinguished in the Tm  
 range of 50-66 degrees C, with success rates of 70% for Exo-PCR and 65%  
 for ss phagemid templates.  
 AB . . . inserts of 1.9, 2.3, 3.8, and 4.9 kbp. Full-length sequences were  
 obtained from both strands of each subclone by automated **dye**  
 -terminator fluorescent DNA sequencing using DENS with degenerate octamer  
**primers**. We compared the following types of DNA templates:  
 single-stranded and double-stranded phagemid DNA, double-stranded PCR  
 products, **asymmetric PCR** products, and single-stranded  
 DNA produced by digestion with Lambda Exonuclease of double-stranded PCR  
 product phosphorylated at one end (Exo-PCR). While. . .  
 L5 ANSWER 6 OF 11 MEDLINE DUPLICATE 2  
 AN 1999010071 MEDLINE  
 DN 99010071 PubMed ID: 9793656  
 TI Detection of **asymmetric PCR** products in homogeneous  
 solution by fluorescence correlation spectroscopy.  
 AU Kinjo M

CS Laboratory of Biophysics, Hokkaido University, Sapporo, Japan.  
SO BIOTECHNIQUES, (1998 Oct) 25 (4) 706-12, 714-5.  
Journal code: AN3; 8306785. ISSN: 0736-6205.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals  
EM 199812  
ED Entered STN: 19990115  
Last Updated on STN: 19990115  
Entered Medline: 19981230

AB The yield of the double-stranded DNA product (500 bp) of **asymmetric PCR** with a rhodamine-labeled **primer** (Rho-primer) was determined in a homogeneous solution using fluorescence correlation spectroscopy (FCS). FCS provides the average number of molecules in a focused volume and the diffusion constant that relates the molecular weight. Since FCS measures the fluctuation of fluorescence intensity in a very small sample volume, the reaction mixture was directly placed on the FCS optical field without any purification procedure after amplification. The result of changing the initial number of templates suggested that elongation of the Rho-primer could be detected by FCS in a PCR mixture containing a single copy of the target gene in the initial condition. Possible scientific applications and perspectives of the proposed approach are discussed.

TI Detection of **asymmetric PCR** products in homogeneous solution by fluorescence correlation spectroscopy.

AB The yield of the double-stranded DNA product (500 bp) of **asymmetric PCR** with a rhodamine-labeled **primer** (Rho-primer) was determined in a homogeneous solution using fluorescence correlation spectroscopy (FCS). FCS provides the average number of molecules in a . . .

L5 ANSWER 7 OF 11 MEDLINE DUPLICATE 3  
AN 1998110314 MEDLINE  
DN 98110314 PubMed ID: 9448847  
TI Integrated amplification and detection of the C677T point mutation in the methylenetetrahydrofolate reductase gene by fluorescence resonance energy transfer and probe melting curves.  
AU Bernard P S; Lay M J; Wittwer C T  
CS Department of Pathology, University of Utah Medical School, Salt Lake City 84132, USA.  
SO ANALYTICAL BIOCHEMISTRY, (1998 Jan 1) 255 (1) 101-7.  
Journal code: 4NK; 0370535. ISSN: 0003-2697.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals  
EM 199803  
ED Entered STN: 19980410  
Last Updated on STN: 19980410  
Entered Medline: 19980327

AB A microvolume fluorimeter integrated with a rapid thermal cycler allows both amplification and point mutation detection from genomic DNA in approximately 30 min. This homogeneous method combines rapid cycle DNA amplification with allele-specific fluorescent probe melting profiles for product genotyping. The amplification reaction includes a **primer** internally labeled with Cy5 and a 3'-fluorescein-labeled probe that spans the region of interest. During **asymmetric amplification**, the probe hybridizes to excess Cy5-labeled strand and is observed as fluorescence resonance energy transfer. Resonance energy transfer increases each cycle as product accumulates during amplification. When fluorescence is monitored as the temperature increases through the T<sub>m</sub> of the probe/product duplex, a characteristic melting profile for each genotype is obtained. Fluorescence genotyping of the

common C677T base substitution in the methylenetetrahydrofolate reductase gene in 110 DNA samples correlated perfectly with genotyping by restriction enzyme digestion and gel electrophoresis. The relatively stable G:T mismatch of this example gave a 3 degrees C difference in T<sub>m</sub> from complete Watson-Crick pairing, suggesting that this homogeneous fluorescence method can be used for all single-base mismatches.

AB . . . . method combines rapid cycle DNA amplification with allele-specific fluorescent probe melting profiles for product genotyping. The amplification reaction includes a **primer** internally labeled with Cy5 and a 3'-fluorescein-labeled probe that spans the region of interest. During **asymmetric amplification**, the probe hybridizes to excess Cy5-labeled strand and is observed as fluorescence resonance energy transfer. Resonance energy transfer increases each. . . .

L5 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2001 ACS

AN 1993:574886 CAPLUS

DN 119:174886

TI Rapid sequencing of unpurified PCR products by thermal **asymmetric** PCR cycle sequencing using unlabeled sequencing primers

AU Liu, Yao Guang; Mitsukawa, Norihiro; Whittier, Robert F.

CS Mitsui Plant Biotechnol. Res. Inst., RITE, Tsukuba, 305, Japan

SO Nucleic Acids Res. (1993), 21(14), 3333-4

CODEN: NARHAD; ISSN: 0305-1048

DT Journal

LA English

AB A new sequencing strategy which omits PCR product purifn., yet does not require end-labeled **primers** for generating clear sequencing ladders is reported. The strategy relies on thermal asym. PCR and utilizes one or two relatively short primers in the initial PCR amplification of target DNA. Subsequent sequencing is carried out by temp. cycling using a longer sequencing primer. Sequencing cycles employ a high annealing temp. to avoid annealing and elongation of carried-over short primers. Sequencing by this strategy is reproducible and reliable without requiring reoptimization of conditions for each new PCR product, and the sequencing quality is as good as with purified samples. In most cases sequence detn. is limited only by the resolving power of the gel.

TI Rapid sequencing of unpurified PCR products by thermal **asymmetric** PCR cycle sequencing using unlabeled sequencing primers

AB A new sequencing strategy which omits PCR product purifn., yet does not require end-labeled **primers** for generating clear sequencing ladders is reported. The strategy relies on thermal asym. PCR and utilizes one or two relatively short primers in the initial PCR amplification of target DNA. Subsequent sequencing is carried out by temp. cycling using a longer sequencing primer. Sequencing cycles employ a high annealing temp. to avoid annealing and elongation of carried-over short primers. Sequencing by this strategy is reproducible and reliable without requiring reoptimization of conditions for each new PCR product, and the sequencing quality is as good as with purified samples. In most cases sequence detn. is limited only by the resolving power of the gel.

L5 ANSWER 9 OF 11 MEDLINE

DUPLICATE 4

AN 92225344 MEDLINE

DN 92225344 PubMed ID: 1563631

TI A rapid polymerase-chain-reaction-directed sequencing strategy using a thermostable DNA polymerase from *Thermus flavus*.

AU Rao V B; Saunders N B

CS Department of Biology, Catholic University of America, Washington, DC 20064.

SO GENE, (1992 Apr 1) 113 (1) 17-23.

Journal code: FOP; 7706761. ISSN: 0378-1119.

CY Netherlands

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals  
 EM 199205  
 ED Entered STN: 19920607  
 Last Updated on STN: 19980206  
 Entered Medline: 19920520

AB We have developed a polymerase chain reaction (PCR)-directed sequencing strategy for rapid sequencing of DNA from crude viral or cell preparations. The basic strategy consists of two phases. In the first phase, the target DNA is amplified by symmetric PCR with low concentrations of deoxyribonucleotide triphosphate (dNTP) and oligodeoxyribonucleotide primers. This results in exponential amplification of DNA in the initial cycles, reaching a plateau by 25 cycles due to limiting concentrations of dNTP and primers. In the second phase, a small aliquot of the PCR mixture is amplified without any purification, by **asymmetric PCR** in the presence of a 5'-labeled primer and one of the four dideoxyribonucleotide triphosphates. This results in the accumulation of single-stranded DNA products that are terminated at specific points by incorporation of the appropriate dideoxyribonucleotide monophosphate. The products are then analyzed by electrophoresis on a sequencing gel followed by autoradiography. The PCR conditions are optimized to generate sequence ladders of several hundred nucleotides starting from as low as 100 copies of bacteriophage or bacterial genome in one to two days.

AB . . . dNTP and primers. In the second phase, a small aliquot of the PCR mixture is amplified without any purification, by **asymmetric PCR** in the presence of a 5'-labeled primer and one of the four dideoxyribonucleotide triphosphates. This results in the accumulation of single-stranded DNA products that are terminated at. . .

L5 ANSWER 10 OF 11 BIOSIS COPYRIGHT 2001 BIOSIS  
 AN 1992:429037 BIOSIS  
 DN BA94:81162  
 TI HIGH-THROUGHPUT FLUORESCENT DNA SEQUENCE ANALYSIS METHODS AND AUTOMATION.  
 AU WILSON R K; HOOD L  
 CS DEP. GENET., WASHINGTON UNIV. SCH. MED., 660 S. EUCLID AVE., ST. LOUIS, MO. 63110, USA.  
 SO METHODS (ORLANDO), (1991) 3 (1), 48-54.  
 CODEN: MTHDE9. ISSN: 1046-2023.

FS BA; OLD  
 LA English

AB A strategy for high-throughput DNA sequence analysis using the fluorescent **dye-primer** chemistry is described. This strategy combines rapid preparation of template DNA using a modification of the polymerase chain reaction (PCR), automation of the DNA sequencing reactions using a robotic laboratory workstation, and subsequent analysis of the fluorescent-labeled reaction products on a commercial automated fluorescent sequencer. **Asymmetric PCR** provides a reliable means of simultaneously producing sufficient and uniform quantities of several template DNAs directly from bacterial colonies or bacteriophage plaques. The automation scheme for subsequent processing and analysis of DNA samples allows a DNA sequencing facility to operate the fluorescent sequencer twice daily at its full capacity of 24 samples. Furthermore, the methods and instruments described eliminate much of the labor required by technicians to obtain a high level of data output. As described here, a DNA sequencing laboratory equipped with a single automated fluorescent sequencer can perform analysis of up to 48 fluorescent-labeled reactions every day, with an average output of over 10,000 bp per sequence run.

AB A strategy for high-throughput DNA sequence analysis using the fluorescent **dye-primer** chemistry is described. This strategy combines rapid preparation of template DNA using a modification of the polymerase chain reaction (PCR), . . . reactions using a robotic laboratory workstation, and subsequent analysis of the fluorescent-labeled reaction products on a commercial automated fluorescent sequencer.



**Asymmetric PCR** provides a reliable means of simultaneously producing sufficient and uniform quantities of several template DNAs directly from bacterial colonies or. . .

L5 ANSWER 11 OF 11 MEDLINE  
AN 90211914 MEDLINE  
DN 90211914 PubMed ID: 2483662  
TI Optimization strategies for the polymerase chain reaction.  
AU Williams J F  
CS Perkin-Elmer Corporation, Norwalk, CT 06859-0251.  
SO BIOTECHNIQUES, (1989 Jul-Aug) 7 (7) 762-9.  
Journal code: AN3; 8306785. ISSN: 0736-6205.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals  
EM 199005  
ED Entered STN: 19900622  
Last Updated on STN: 19980206  
Entered Medline: 19900514  
AB The GeneAmp polymerase chain reaction (PCR) process has now become a key procedure in molecular biology research laboratories. The PCR technique is an in vitro method in which genomic or cloned target sequences are specifically enzymatically amplified as directed by a pair of oligonucleotide primers. This technique has been quite robust in the hands of the majority of researchers and is extremely flexible, as evidenced by the increasing number of related PCR formats (i.e., inverse PCR, anchored PCR, **asymmetric PCR, labeled primer** PCR and RNA-PCR). Today's applications include direct sequencing, genomic cloning, DNA typing, detection of infectious microorganisms, site-directed mutagenesis, prenatal genetic disease research, and analysis of allelic sequence variations. Scientists at Cetus and Perkin-Elmer have collaborated for several years to better understand the interacting biochemical and biophysical parameters which affect PCR optimization. Following are many of the current recommendations, offered with the caveat that our understanding of the PCR process is continually evolving.  
AB . . . researchers and is extremely flexible, as evidenced by the increasing number of related PCR formats (i.e., inverse PCR, anchored PCR, **asymmetric PCR, labeled primer** PCR and RNA-PCR). Today's applications include direct sequencing, genomic cloning, DNA typing, detection of infectious microorganisms, site-directed mutagenesis, prenatal genetic. . .

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